Application No.: 09/915,515 Docket No.: 21663-00193-US

AMENDMENTS TO THE CLAIMS

Please cancel claim 13 without prejudice to its reentry at some later date.

1. (Currently amended) A method for identifying a potential inhibitor for a paramyxovirus Hemagglutinin-neuraminidase, comprising ~~the steps of:~~

a. ~~using~~ applying a three -dimensional structure of the paramyxovirus ~~hemagglutinen~~ Hemogglutinin-neuraminidase as defined by the structure coordinates comprising the amino acid residues 174, 175, 190, 192, 199, 234, 236, 237, 254, 256, 258, 262, 299, 302, 317, 363, 364, 369, 401, 416, 466, 498, and 526 according to SEQ ID NO: 1;

~~[b. applying the three-dimensional structure~~ to design or select the potential inhibitor;

b. ~~c.~~ containing the potential inhibitor; and

c. ~~d.~~ associating the potential inhibitor with the enzyme in the presence of a substrate to determine the ability of the potential inhibitor to inhibit the enzyme.

2. (Original) The method according to claim 1, wherein the potential inhibitor is designed de novo.

3. (Original) The method according to claim 1, wherein the potential inhibitor is designed from a known inhibitor.

4. (Currently amended) The method according to claim 1, wherein ~~the step of employing~~ applying the three-dimensional structure to design or select the compound comprises [the steps of:]

a. identifying chemical entities or fragments capable of associating with the enzyme; and

b. assembling the identified chemical entities or fragments into a single molecule to provide the structure of the potential inhibitor.

5. (Original) The method of according to claim 4, wherein the potential inhibitor is designed de novo.

6. (Original) The method according to claim 4, wherein the potential inhibitor is designed from a known inhibitor.

7. (Withdrawn) A complex of a paramyxovirus Hemagglutinin-neuraminidase and a substrate or inhibitor molecule.

8. (Withdrawn) The complex of claim 7 being obtained by diffusion or co-crystallization.

9. (Currently amended) The method according to claim 1 wherein the potential inhibitor is a competitive, noncompetitive, or uncompetitive inhibitor of a paramyoxvirus Hemagglutinin neuraminidase ~~HemagglutininNeuraminidase~~.

10. (Currently amended) The method according to claim 1 wherein the potential inhibitor is designed to form salt links with Arg416 and Arg498 of a paramyxovirus Hemagglutinin neuraminidase ~~hemagglutininneuraminidase~~.

11. (Currently amended) The method according to claim 1 wherein the potentail inhibitor is designed to form hydrogen bonds or salt links with Glu258 of a paramyxovirus Hemagglutinin neuraminidase ~~hemagglutininneuraminidase~~.

12. (Currently amended) The method according to claim 1 wherein the potential inhibitor is designed to form hydrogen bonds or salt links with Lys 199 of a paramyxovirus Hemagglutinin neuraminidase ~~hemagglutininneuraminidase~~.

13. (Canceled)

14. (Currently amended) The method of claim [13] 1 wherein the paramyxovirus hemagglutnin-neuraminidase is Neucastle Disease Virus Hemagglutinin ~~hemagglutnin~~ neuraminidase.

15. (Withdrawn) A machine readable data storage medium comprising a data storage material encoded with machine-readable data which comprises the structure coordinates comprising the amino acid residues 174, 175, 190, 192, 199, 234, 236, 237, 254, 256, 258, 262, 299, 302, 317, 363, 364, 369, 401, 416, 466, 498 and 526 according to SEQ ID NO:1.

16. (Withdrawn-Currently amended) The machine-readable data storage medium of claim 15 wherein the machine-readable data comprises the three-dimensional structure of paramyxovirus Hemagglutinin ~~Hemagglutnin~~-neuraminidase.

17. (Withdrawn-Currently amended) The machine-readable data storage medium of claim 16 wherein the paramyxovirus Hemagglutnin-neuraminidase is Newcastle Disease Virus ~~Hemagglutnin~~ Hemagglutinin -Neuraminidase.

18. (Withdrawn) A computer for producing a three-dimensional representation of:

a. a molecule or molecular complex, wherein said molecules or molecular complex comprises a binding pocket defined by structure coordinates comprising the amino acid residues 174, 175, 190, 192, 199, 234, 236, 237, 254, 256, 258, 262, 299, 302, 317, 363, 364, 369, 401, 416, 466, 498 and 526 according to SEQ ID NO:1; wherein the computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, comprising the structure coordinates comprising the amino acid residues 174, 175, 190, 192, 199, 234, 236, 237, 254, 256, 258, 262, 299, 302, 317, 363, 364, 369, 401, 416, 466, 498 and 526 according to SEQ ID NO:1;

(ii) a working memory for storing instructions for processing the machine-readable data;

(iii) a central-processing unit coupled to the working memory and to the machine-readable data storage medium for processing the machine readable data into the three-dimensional representation; and

(iv) a display coupled to the central-processing unit for displaying the three-dimensional representation.

19. (Withdrawn-Currently amended) The computer of claim 18 wherein the computer produces a three-dimensional representation of a paramyxovirus ~~Hemagglutnin~~ Hemagglutinin -neuraminidase; and

wherein the machine-readable data comprises the structure coordinates of paramyxovirus ~~Hemagglutnin~~ Hemagglutinin-neuraminidase.

20. (Withdrawn-Currently amended) The computer of claim 18 wherein the computer produces a three-dimensional representation of Newcastle Disease Virus Hemagglutinin ~~Hemagglutnin~~ Neuraminidase and wherein the machine readable data comprises the structure coordinate of Newcastle Disease Virus Hemagglutinin ~~Hemagglutnin~~ Neuraminidase.

21. (Original) The method of claim 1 which comprises:

employing computational means to perform a fitting operation between the potential inhibitor and the structure coordinates of the three-dimensional structure; and

analyzing the results of the fitting operation to quantify the association between the potential inhibitor and the structure coordinates.